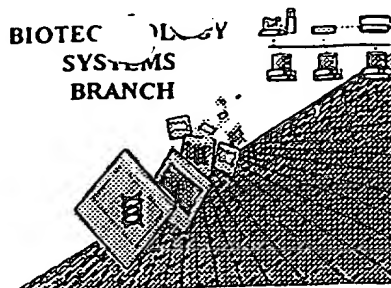


C. Fronda  
RUSH

**RAW SEQUENCE LISTING**  
**ERROR REPORT**



The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/486,247

Source: 1652

Date Processed by STIC: 09/24/2001

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: [patin21help@uspto.gov](mailto:patin21help@uspto.gov) or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: [patin3help@uspto.gov](mailto:patin3help@uspto.gov) or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

### Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 - 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:

<http://www.uspto.gov/web/offices/pac/checker>

1652

## RAW SEQUENCE LISTING

DATE: 09/24/2001

PATENT APPLICATION: US/09/486,247

TIME: 12:08:14

Input Set : A:\8484081999.txt

Output Set: N:\CRF3\09242001\I486247.raw

Does Not Comply  
Corrected Diskette Needed

5 <110> APPLICANT: DEAR, TERENCE N  
7 BOEHM, THOMAS  
11 <120> TITLE OF INVENTION: PROTEASE-RELATED PROTEIN  
15 <130> FILE REFERENCE: 8484-081-999  
19 <140> CURRENT APPLICATION NUMBER: 09/486,247  
21 <141> CURRENT FILING DATE: 2000-05-25  
23 <150> PRIOR APPLICATION NUMBER: DE 197 36 198.6  
24 <151> PRIOR FILING DATE: 1997-08-20  
27 <160> NUMBER OF SEQ ID NOS: 8  
31 <170> SOFTWARE: PatentIn version 3.1  
35 <210> SEQ ID NO: 1  
37 <211> LENGTH: 822  
39 <212> TYPE: DNA  
41 <213> ORGANISM: Artificial Sequence  
45 <220> FEATURE:  
47 <223> OTHER INFORMATION: Description of Artificial Sequence: Polynucleotide  
49 <221> NAME/KEY: CDS  
51 <222> LOCATION: (1)..(822)  
53 <223> OTHER INFORMATION:  
56 <400> SEQUENCE: 1

57	tag	gtg	gtg	tca	ttc	ccc	tcc	aac	ctg	agt	gct	ggc	agg	tac	act	gct	
58		Val	Val	Ser	Phe	Pro	Ser	Asn	Leu	Ser	Ala	Gly	Arg	Tyr	Thr	Ala	
59		1				5					10					15	
64	ggc	cac	cag	cag	atg	ccc	atg	aag	atg	ctg	aca	atg	aag	atg	ctg	gcc	
65	Gly	His	Gln	Gln	Met	Pro	Met	Lys	Met	Leu	Thr	Met	Lys	Met	Leu	Ala	
66					20					25					30		
68	ctg	tgc	ttg	gtt	ctt	gct	aaa	tca	gcc	tgg	tcg	gag	gaa	cag	gag	aag	
69	Leu	Cys	Leu	Val	Leu	Ala	Lys	Ser	Ala	Trp	Ser	Glu	Glu	Gln	Glu	Lys	
70					35				40					45			
72	gtg	gtt	cat	gga	ggc	ccg	tgt	ttg	aag	gac	tcc	cac	cct	ttc	cag	gct	
73	Val	Val	His	Gly	Gly	Pro	Cys	Leu	Lys	Asp	Ser	His	Pro	Phe	Gln	Ala	
74			50					55					60				
76	gcc	ctc	tac	acc	tca	ggt	cac	ttg	ctg	tgt	ggt	ggg	gtc	ctc	att	gac	240
77	Ala	Leu	Tyr	Thr	Ser	Gly	His	Leu	Leu	Cys	Gly	Gly	Val	Leu	Ile	Asp	
78		65					70				75						
80	cca	cag	tgg	gtg	ctg	aca	gct	gcc	cac	tgc	aaa	aaa	ccg	aat	ctg	cag	288
81	Pro	Gln	Trp	Val	Leu	Thr	Ala	Ala	His	Cys	Lys	Lys	Pro	Asn	Leu	Gln	
82	80					85				90					95		
84	gtg	atc	ttg	ggg	aaa	cac	aac	cta	cgg	caa	aca	gag	act	ttc	caa	agg	336
85	Val	Ile	Leu	Gly	Lys	His	Asn	Leu	Arg	Gln	Thr	Glu	Thr	Phe	Gln	Arg	
86				100					105					110			
88	caa	atc	tca	gtg	gac	agg	act	att	gtc	cat	ccc	cgc	tac	aac	cct	gaa	384
89	Gln	Ile	Ser	Val	Asp	Arg	Thr	Ile	Val	His	Pro	Arg	Tyr	Asn	Pro	Glu	
90				115					120					125			
92	acc	cac	gac	aat	gac	atc	atg	atg	gtg	cat	ctg	aaa	aat	cca	gtc	aaa	432
93	Thr	His	Asp	Asn	Asp	Ile	Met	Met	Val	His	Leu	Lys	Asn	Pro	Val	Lys	
94			130					135						140			

Polynucleotide

need to indicate  
the source of  
the Genetic  
material.  
See item 11 on  
Error Summary  
Sheet

## RAW SEQUENCE LISTING

DATE: 09/24/2001

PATENT APPLICATION: US/09/486,247

TIME: 12:08:14

Input Set : A:\8484081999.txt

Output Set: N:\CRF3\09242001\I486247.raw

```

96 .ttc tct aaa aag atc cag cct ctg ccc ttg aag aat gac tgc tct gag      480
97 Phe Ser Lys Lys Ile Gln Pro Leu Pro Leu Lys Asn Asp Cys Ser Glu
98      145                      150                      155
100 gag aat ccc aac tgc cag atc ctg ggc tgg ggc aag atg gaa aat ggt      528
101 Glu Asn Pro Asn Cys Gln Ile Leu Gly Trp Gly Lys Met Glu Asn Gly
102 160                      165                      170                      175
104 gac ttc cca gat acc att cag tgt gct gat gtc cat ctg gtg ccc cgg      576
105 Asp Phe Pro Asp Thr Ile Gln Cys Ala Asp Val His Leu Val Pro Arg
106                      180                      185                      190
108 gag cag tgt gag cgt gcc tac cct ggc aag atc acc cag agc atg gtg      624
109 Glu Gln Cys Glu Arg Ala Tyr Pro Gly Lys Ile Thr Gln Ser Met Val
110                      195                      200                      205
112 tgc gca ggc gac atg aaa gaa ggc aac gat tcc tgt cag ggt gat tct      672
113 Cys Ala Gly Asp Met Lys Glu Gly Asn Asp Ser Cys Gln Gly Asp Ser
114      210                      215                      220
116 gga ggt ccc cta gta tgt ggg ggt cgc ctc cga ggg ctc gtg tca tgg      720
117 Gly Gly Pro Leu Val Cys Gly Gly Arg Leu Arg Gly Leu Val Ser Trp
118      225                      230                      235
120 ggt gac atg ccc tgt gga tca aag gag aag cca gga gtt tac acc gat      768
121 Gly Asp Met Pro Cys Gly Ser Lys Glu Lys Pro Gly Val Tyr Thr Asp
122 240                      245                      250                      255
126 gtc tgc act cat atc aga tgg atc caa aac atc ctc aga aac aag tgg      816
127 Val Cys Thr His Ile Arg Trp Ile Gln Asn Ile Leu Arg Asn Lys Trp
128                      260                      265                      270
130 ctg tga      822
131 Leu
134 <210> SEQ ID NO: 2
136 <211> LENGTH: 272
138 <212> TYPE: PRT
140 <213> ORGANISM: Artificial Sequence
142 <220> FEATURE:
144 <223> OTHER INFORMATION: Description of Artificial Sequence: Polynucleotide
146 <400> SEQUENCE: 2
148 Val Val Ser Phe Pro Ser Asn Leu Ser Ala Gly Arg Tyr Thr Ala Gly
149 1                      5                      10                      15
152 His Gln Gln Met Pro Met Lys Met Leu Thr Met Lys Met Leu Ala Leu
153      20                      25                      30
156 Cys Leu Val Leu Ala Lys Ser Ala Trp Ser Glu Glu Gln Glu Lys Val
157      35                      40                      45
160 Val His Gly Gly Pro Cys Leu Lys Asp Ser His Pro Phe Gln Ala Ala
161      50                      55                      60
164 Leu Tyr Thr Ser Gly His Leu Leu Cys Gly Gly Val Leu Ile Asp Pro
165 65                      70                      75                      80
168 Gln Trp Val Leu Thr Ala Ala His Cys Lys Lys Pro Asn Leu Gln Val
169      85                      90                      95
172 Ile Leu Gly Lys His Asn Leu Arg Gln Thr Glu Thr Phe Gln Arg Gln
173      100                      105                      110
176 Ile Ser Val Asp Arg Thr Ile Val His Pro Arg Tyr Asn Pro Glu Thr
177      115                      120                      125

```

1  
This is not  
polynucleotide

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/486,247

DATE: 09/24/2001

TIME: 12:08:14

Input Set : A:\8484081999.txt

Output Set: N:\CRF3\09242001\I486247.raw

180 His Asp Asn Asp Ile Met Met Val His Leu Lys Asn Pro Val Lys Phe  
 181 130 135 140  
 185 Ser Lys Lys Ile Gln Pro Leu Pro Leu Lys Asn Asp Cys Ser Glu Glu  
 186 145 150 155 160  
 189 Asn Pro Asn Cys Gln Ile Leu Gly Trp Gly Lys Met Glu Asn Gly Asp  
 190 165 170 175  
 193 Phe Pro Asp Thr Ile Gln Cys Ala Asp Val His Leu Val Pro Arg Glu  
 194 180 185 190  
 198 Gln Cys Glu Arg Ala Tyr Pro Gly Lys Ile Thr Gln Ser Met Val Cys  
 199 195 200 205  
 202 Ala Gly Asp Met Lys Glu Gly Asn Asp Ser Cys Gln Gly Asp Ser Gly  
 203 210 215 220  
 206 Gly Pro Leu Val Cys Gly Gly Arg Leu Arg Gly Leu Val Ser Trp Gly  
 207 225 230 235 240  
 210 Asp Met Pro Cys Gly Ser Lys Glu Lys Pro Gly Val Tyr Thr Asp Val  
 211 245 250 255  
 214 Cys Thr His Ile Arg Trp Ile Gln Asn Ile Leu Arg Asn Lys Trp Leu  
 215 260 265 270

218 &lt;210&gt; SEQ ID NO: 3

220 &lt;211&gt; LENGTH: 12

222 &lt;212&gt; TYPE: DNA

224 &lt;213&gt; ORGANISM: Artificial Sequence

226 &lt;220&gt; FEATURE:

228 &lt;223&gt; OTHER INFORMATION: Description of Artificial Sequence: Polynucleotide

230 &lt;400&gt; SEQUENCE: 3

231 gatctgcggt ga

12

234 &lt;210&gt; SEQ ID NO: 4

236 &lt;211&gt; LENGTH: 24

238 &lt;212&gt; TYPE: DNA

240 &lt;213&gt; ORGANISM: Artificial Sequence

242 &lt;220&gt; FEATURE:

244 &lt;223&gt; OTHER INFORMATION: Description of Artificial Sequence: Polynucleotide

246 &lt;400&gt; SEQUENCE: 4

247 agcactctcc agcctctcac cgca

24

250 &lt;210&gt; SEQ ID NO: 5

252 &lt;211&gt; LENGTH: 12

254 &lt;212&gt; TYPE: DNA

256 &lt;213&gt; ORGANISM: Artificial Sequence

258 &lt;220&gt; FEATURE:

260 &lt;223&gt; OTHER INFORMATION: Description of Artificial Sequence: Polynucleotide

263 &lt;400&gt; SEQUENCE: 5

264 gatctgttca tg

12

267 &lt;210&gt; SEQ ID NO: 6

269 &lt;211&gt; LENGTH: 24

271 &lt;212&gt; TYPE: DNA

273 &lt;213&gt; ORGANISM: Artificial Sequence

275 &lt;220&gt; FEATURE:

277 &lt;223&gt; OTHER INFORMATION: Description of Artificial Sequence: Polynucleotide

279 &lt;400&gt; SEQUENCE: 6

See page 1

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/486,247

DATE: 09/24/2001

TIME: 12:08:14

Input Set : A:\8484081999.txt

Output Set: N:\CRF3\09242001\I486247.raw

280 accgacgtcg actatccatg aaca 24  
283 <210> SEQ ID NO: 7  
285 <211> LENGTH: 12  
287 <212> TYPE: DNA  
289 <213> ORGANISM: Artificial Sequence  
291 <220> FEATURE:  
293 <223> OTHER INFORMATION: Description of Artificial Sequence: Polynucleotide  
295 <400> SEQUENCE: 7  
296 gatcttccct cg 12  
299 <210> SEQ ID NO: 8  
301 <211> LENGTH: 24  
303 <212> TYPE: DNA  
305 <213> ORGANISM: Artificial Sequence  
307 <220> FEATURE:  
309 <223> OTHER INFORMATION: Description of Artificial Sequence: Polynucleotide  
312 <400> SEQUENCE: 8  
313 aggcaactgt gctatccgag ggaa 24

1  
see page 1

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/486,247

DATE: 09/24/2001

TIME: 12:08:15

Input Set : A:\8484081999.txt

Output Set: N:\CRF3\09242001\I486247.raw

**NOTICE TO COMPLY WITH REQUIREMENTS FOR PATENT APPLICATIONS CONTAINING  
NUCLEOTIDE SEQUENCE AND/OR AMINO ACID SEQUENCE DISCLOSURES**

Applicant must file the items indicated below within the time period set the Office action to which the Notice is attached to avoid abandonment under 35 U.S.C. § 133 (extensions of time may be obtained under the provisions of 37 CFR 1.136(a)).

The nucleotide and/or amino acid sequence disclosure contained in this application does not comply with the requirements for such a disclosure as set forth in 37 C.F.R. 1.821 - 1.825 for the following reason(s):

- ☐ 1. This application clearly fails to comply with the requirements of 37 C.F.R. 1.821-1.825. Applicant's attention is directed to the final rulemaking notice published at 55 FR 18230 (May 1, 1990), and 1114 OG 29 (May 15, 1990). If the effective filing date is on or after July 1, 1998, see the final rulemaking notice published at 63 FR 29620 (June 1, 1998) and 1211 OG 82 (June 23, 1998).
- ☐ 2. This application does not contain, as a separate part of the disclosure on paper copy, a "Sequence Listing" as required by 37 C.F.R. 1.821(c).
- ☐ 3. A copy of the "Sequence Listing" in computer readable form has not been submitted as required by 37 C.F.R. 1.821(e).
- ☒ 4. A copy of the "Sequence Listing" in computer readable form has been submitted. However, the content of the computer readable form does not comply with the requirements of 37 C.F.R. 1.822 and/or 1.823, as indicated on the attached copy of the marked -up "Raw Sequence Listing."
- ☐ 5. The computer readable form that has been filed with this application has been found to be damaged and/or unreadable as indicated on the attached CRF Diskette Problem Report. A Substitute computer readable form must be submitted as required by 37 C.F.R. 1.825(d).
- ☐ 6. The paper copy of the "Sequence Listing" is not the same as the computer readable form of the "Sequence Listing" as required by 37 C.F.R. 1.821(e).
- ☐ 7. Other: \_\_\_\_\_

**Applicant Must Provide:**

- ☒ An substitute computer readable form (CRF) copy of the "Sequence Listing".
- ☒ An substitute paper copy of the "Sequence Listing", as well as an amendment directing its entry into the specification.
- ☒ A statement that the content of the paper and computer readable copies are the same and, where applicable, include no new matter, as required by 37 C.F.R. 1.821(e) or 1.821(f) or 1.821(g) or 1.825(b) or 1.825(d).

For questions regarding compliance to these requirements, please contact:

For Rules Interpretation, call (703) 308-4216

For CRF Submission Help, call (703) 308-4212

PatentIn Software Program Support

Technical Assistance.....703-287-0200

To Purchase PatentIn Software.....703-306-2600

**PLEASE RETURN A COPY OF THIS NOTICE WITH YOUR REPLY**

## Raw Sequence Listing Error Summary

### ERROR DETECTED

### SUGGESTED CORRECTION

SERIAL NUMBER: 09/486,247

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1      Wrapped Nucleics  
    Wrapped Aminos     The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
  
- 2      Invalid Line Length     The rules require that a line not exceed 72 characters in length. This includes white spaces.
  
- 3      Misaligned Amino  
    Numbering     The numbering under each 5<sup>th</sup> amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.
  
- 4      Non-ASCII     The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
  
- 5      Variable Length     Sequence(s)      contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
  
- 6      PatentIn 2.0  
    "bug"     A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s)     . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
  
- 7      Skipped Sequences  
    (OLD RULES)     Sequence(s)      missing. If intentional, please insert the following lines for each skipped sequence:  
                                   (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)  
                                   (i)     SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)  
                                   (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)  
                                   This sequence is intentionally skipped  
  
                                   Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
  
- 8      Skipped Sequences  
    (NEW RULES)     Sequence(s)      missing. If intentional, please insert the following lines for each skipped sequence.  
                                   <210> sequence id number  
                                   <400> sequence id number  
                                   000
  
- 9      Use of n's or Xaa's  
    (NEW RULES)     Use of n's and/or Xaa's have been detected in the Sequence Listing.  
                                   Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.  
                                   In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
  
- 10      Invalid <213>  
    Response     Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence
  
- 11      Use of <220>     Sequence(s)      missing the <220> "Feature" and associated numeric identifiers and responses.  
                                   Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.  
                                   (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
  
- 12      PatentIn 2.0  
    "bug"     Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.